

## IN THE SPECIFICATION

Please replace the paragraph beginning on page 18, line 19 with the following:

Similarity analysis includes database search and alignment. Examples of public databases include the DNA Database of Japan (DDBJ)(available on the worldwide web at <http://www.ddbj.nig.ac.jp/>); Genebank (available on the worldwide web at the ncbi website at: <http://www.ncbi.nlm.nih.gov/Web/Search/Index.html>); and the European Molecular Biology Laboratory Nucleic Acid Sequence Database (EMBL) ([http://www.ebi.ac.uk/ebi\\_docs/embl\\_db/embl-db.html](http://www.ebi.ac.uk/ebi_docs/embl_db/embl-db.html)). Other appropriate databases include dbEST (<http://www.ncbi.nlm.nih.gov/dbEST/index.html>), SwissProt ([http://www.ebi.ac.uk/ebi\\_docs/swisprot\\_db/swisshome.html](http://www.ebi.ac.uk/ebi_docs/swisprot_db/swisshome.html)), PIR (<http://www.nbrt.georgetown.edu/pir/>) and The Institute for Genome Research (<http://www.tigr.org/tdb/tdb.html>).

Please replace the paragraph beginning on page 20 line 18 with the following:

Homologues in other organisms are available that can be used for comparative sequence analysis. Multiple alignments are performed to study similarities and differences in a group of related sequences. CLUSTAL W is a multiple sequence alignment package that performs progressive multiple sequence alignments based on the method of Feng and Doolittle, *J. Mol. Evol.* 25:351-360 (1987), the entirety of which is herein incorporated by reference. Each pair of sequences is aligned and the distance

between each pair is calculated; from this distance matrix, a guide tree is calculated and all of the sequences are progressively aligned based on this tree. A feature of the program is its sensitivity to the effect of gaps on the alignment; gap penalties are varied to encourage the insertion of gaps in probable loop regions instead of in the middle of structured regions. Users can specify gap penalties, choose between a number of scoring matrices, or supply their own scoring matrix for both pairwise alignments and multiple alignments. CLUSTAL W for UNIX and VMS systems is available at the ftp site: ~~ebi.ac.uk. ÷ ftp.ebi.ac.uk.~~ Another program is MACAW (Schuler *et al.*, *Proteins Struct. Func. Genet.* 9:180-190 (1991), the entirety of which is herein incorporated by reference, for which both Macintosh and Microsoft Windows versions are available. MACAW uses a graphical interface, provides a choice of several alignment algorithms and is available by anonymous ftp available at the ncbi website at ~~directory/pub/macaw. ÷ ncbi.nlm.nih.gov (directory/pub/macaw).~~